FIG. 1

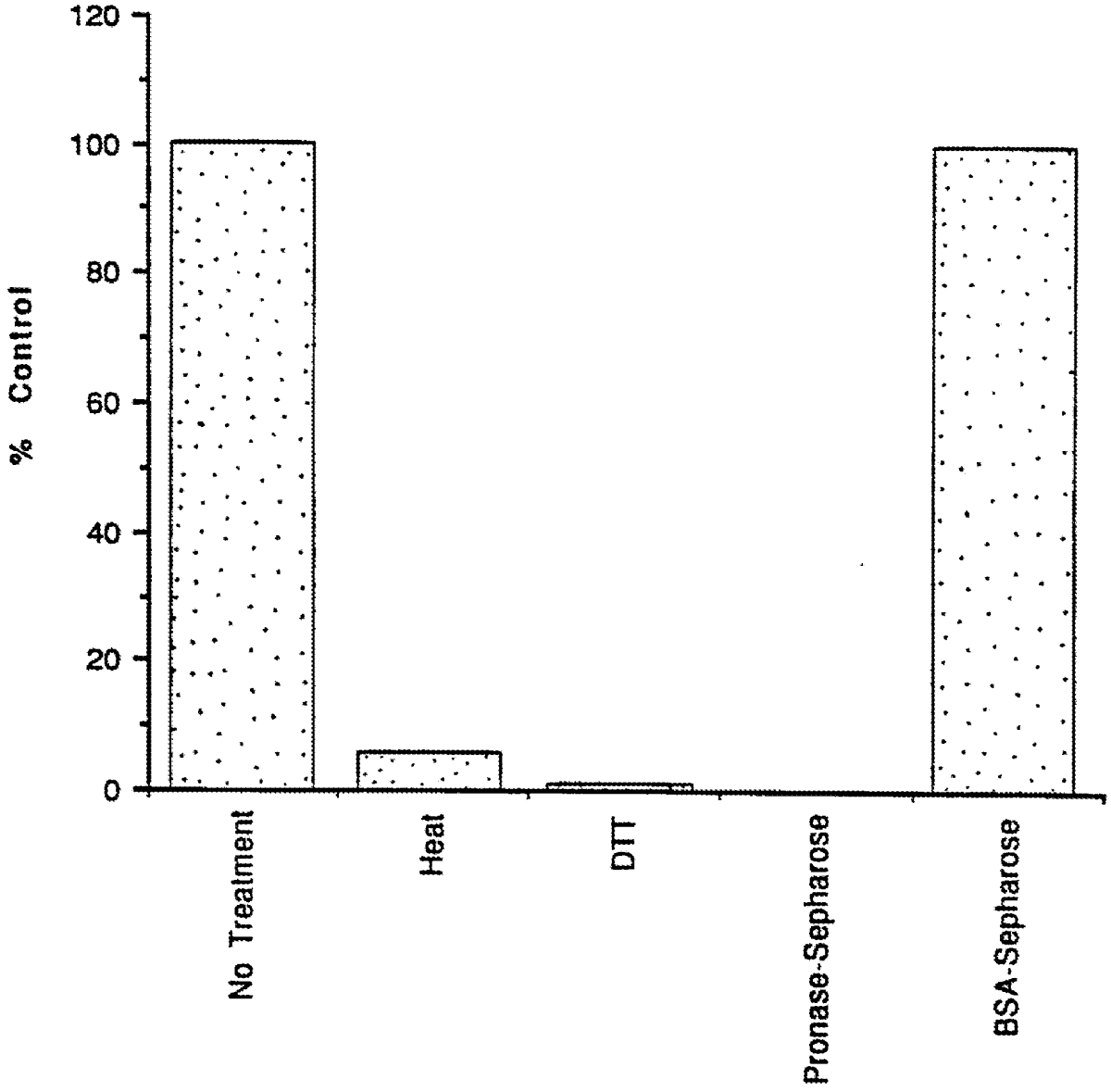

120
100
80
60
40
20
0
% Control
No Treatment
Heat
DTT
Pronase-Sepharose
BSA-Sepharose

FIG. 2

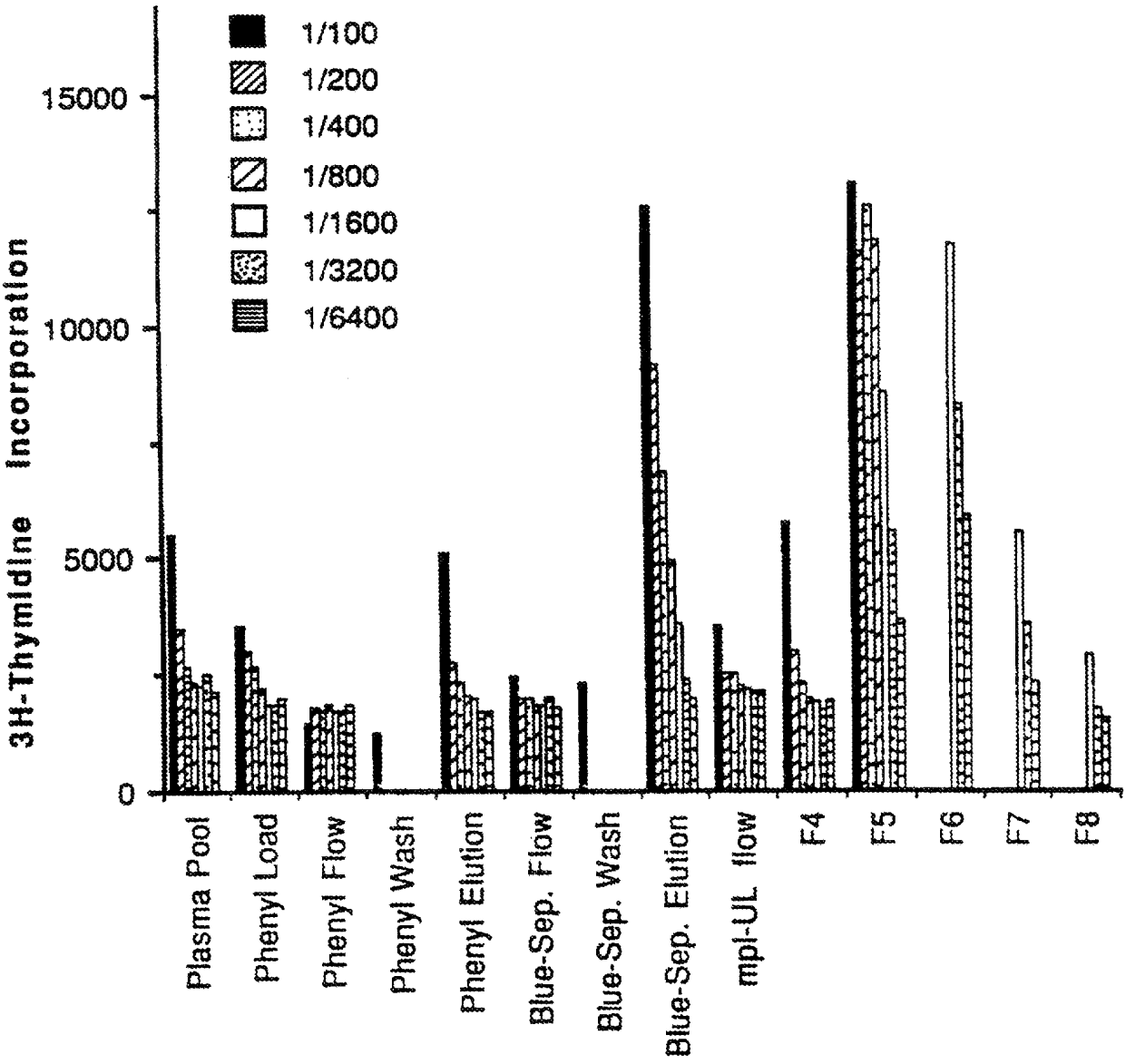

1/100
1/200
1/400
1/800
1/1600
1/3200
1/6400
3H-Thymidine Incorporation
15000
10000
5000
0
Plasma Pool
Phenyl Load
Phenyl Flow
Phenyl Wash
Phenyl Elution
Blue-Sep. Flow
Blue-Sep. Wash
Blue-Sep. Elution
mpl-UL flow
F4
F5
F6
F7
F8

FIG. 3

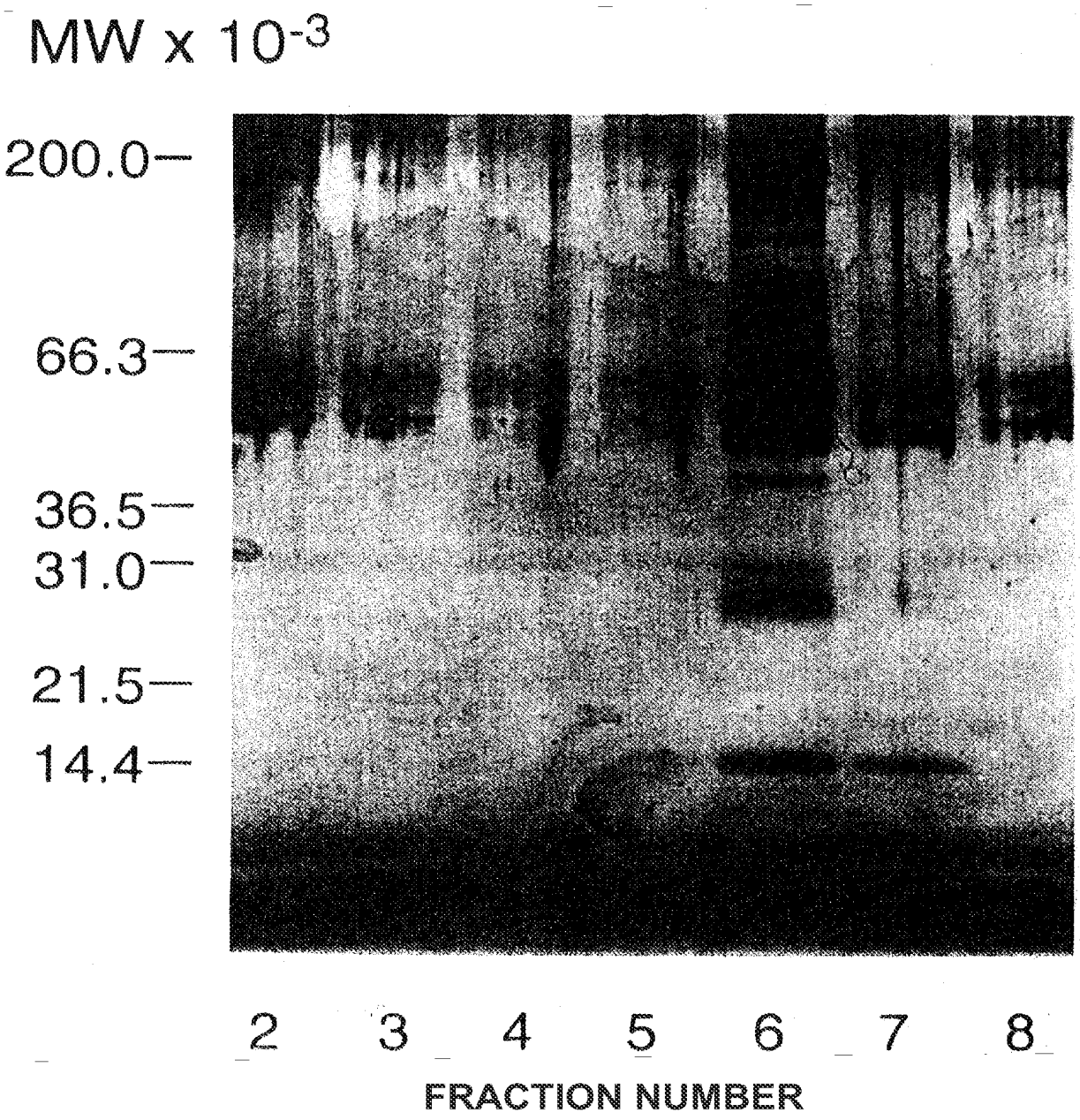


FIG. 4

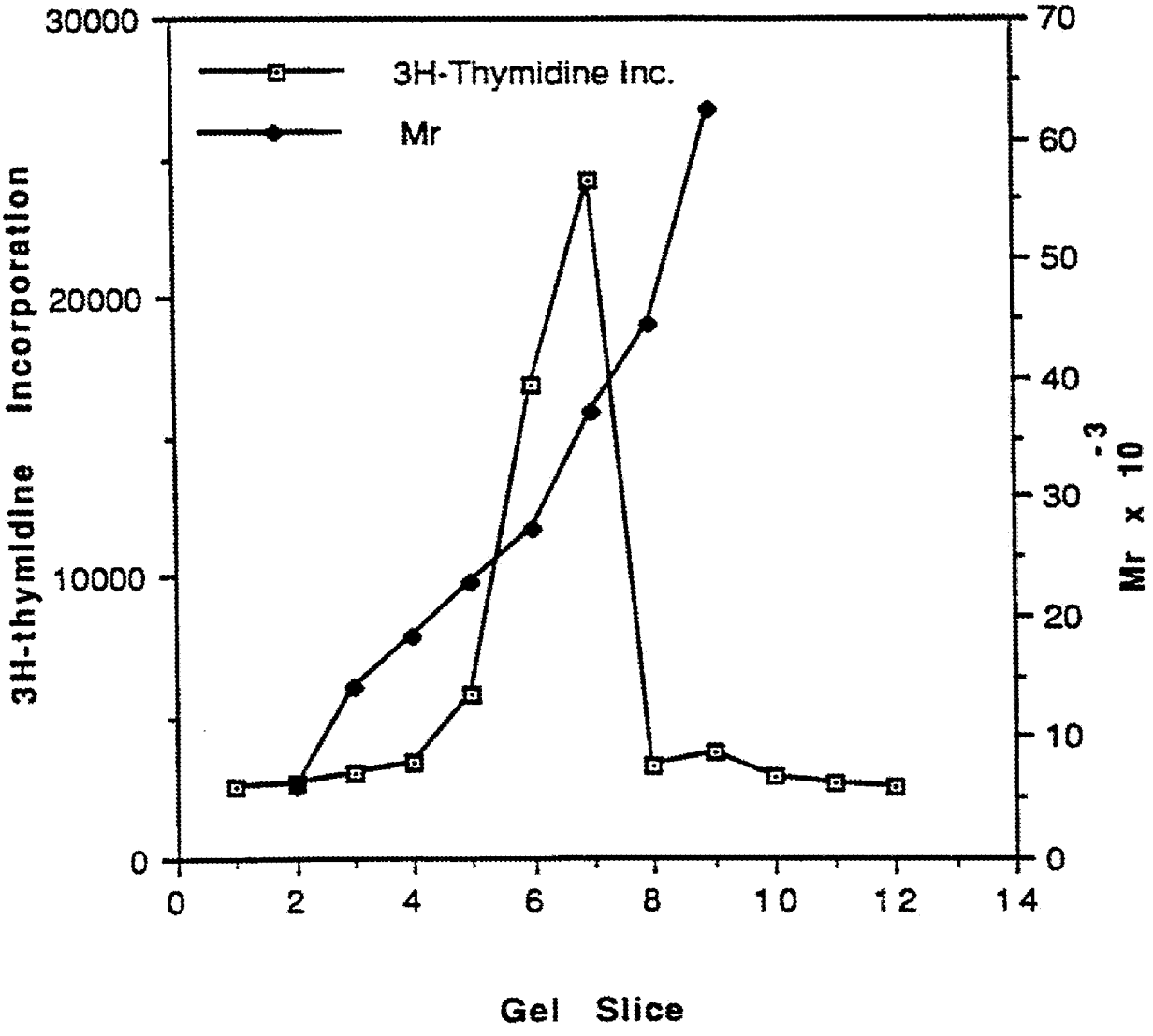

30000
20000
10000
0
70
60
50
40
30
20
10
0
0
2
4
6
8
10
12
14
3H-Thymidine Inc.
Mr
3H-thymidine Incorporation
Mr x 10 -3
Gel Slice

FIG. 5

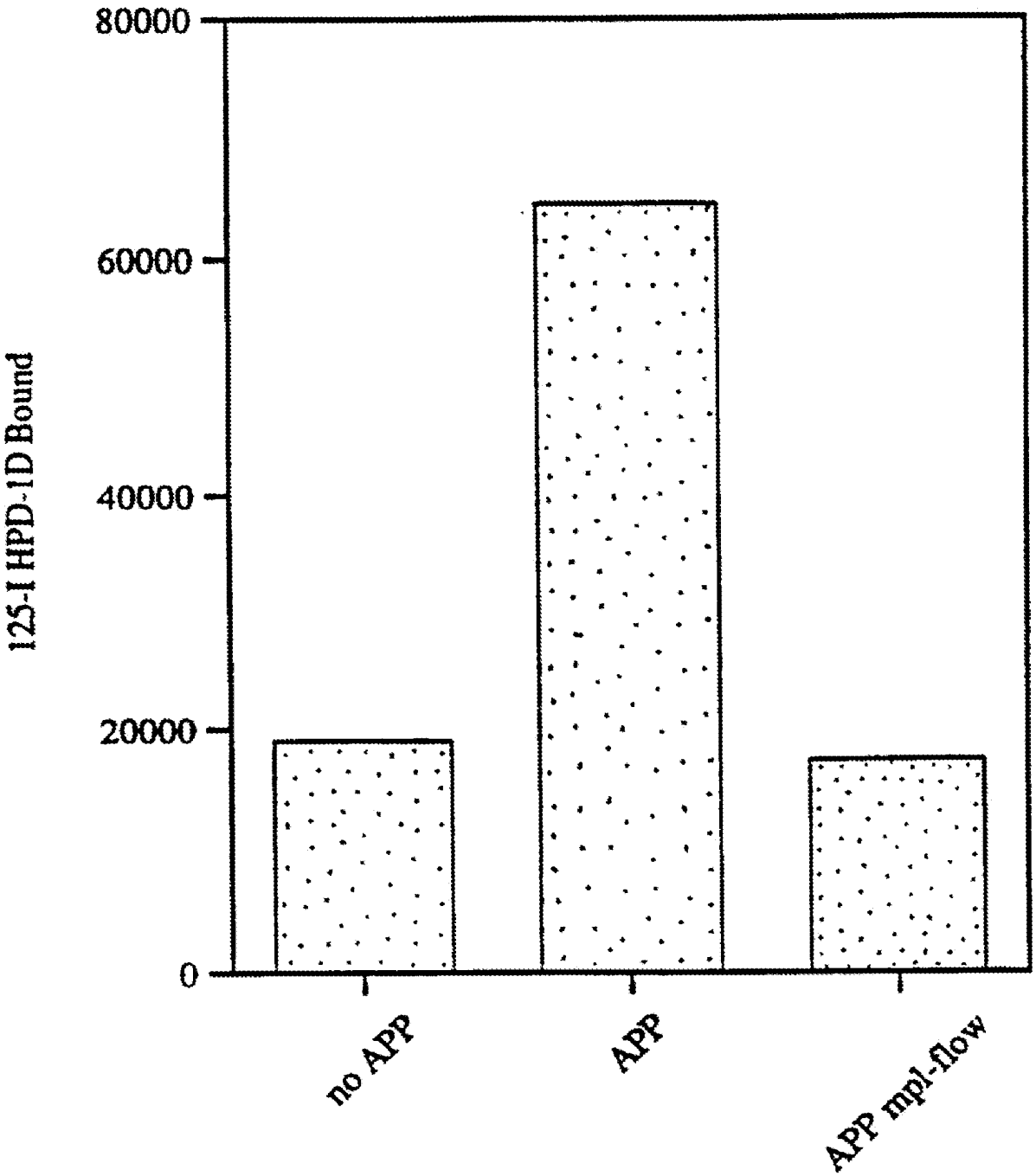

80000
60000
40000
20000
0
125-I HPD-1D Bound
no APP
APP
APP mpl-flow

FIG. 6

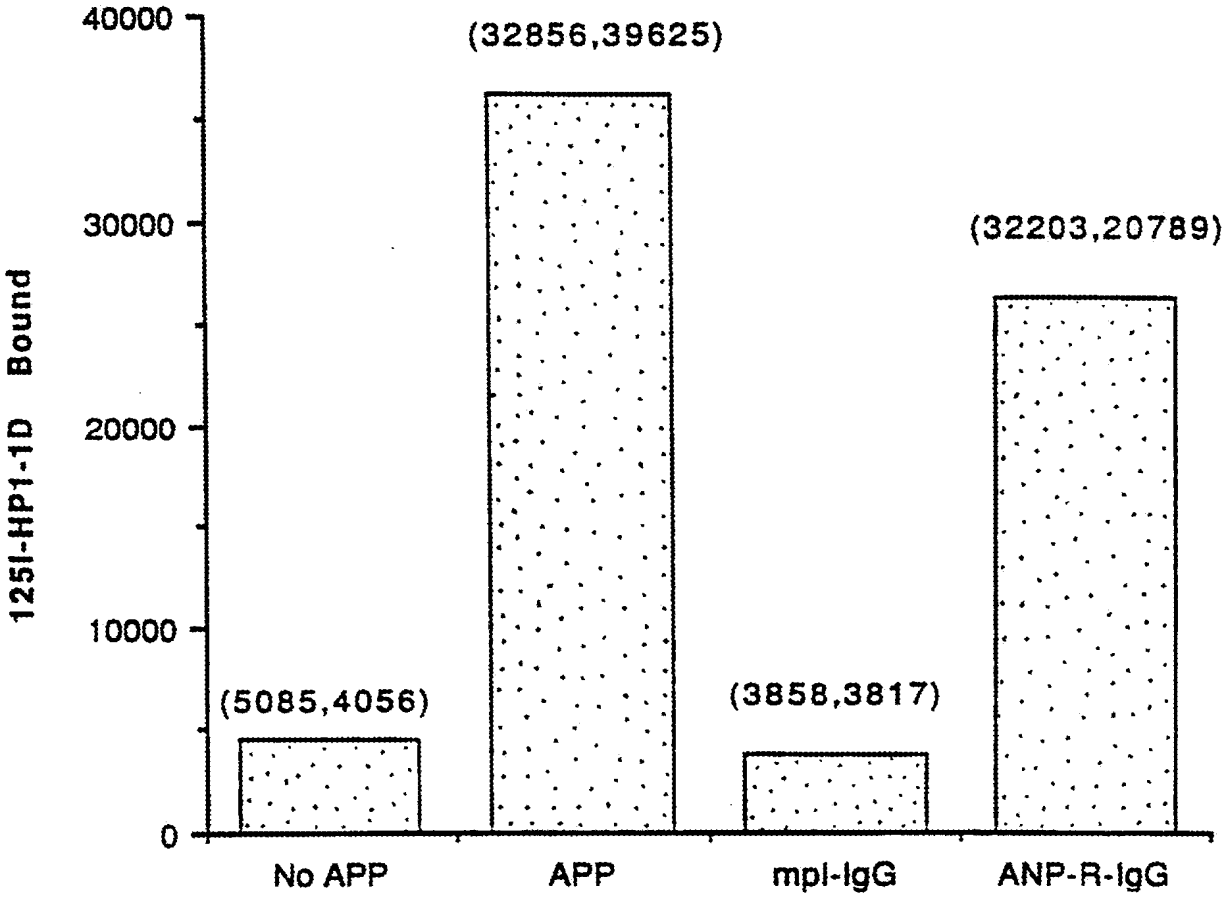
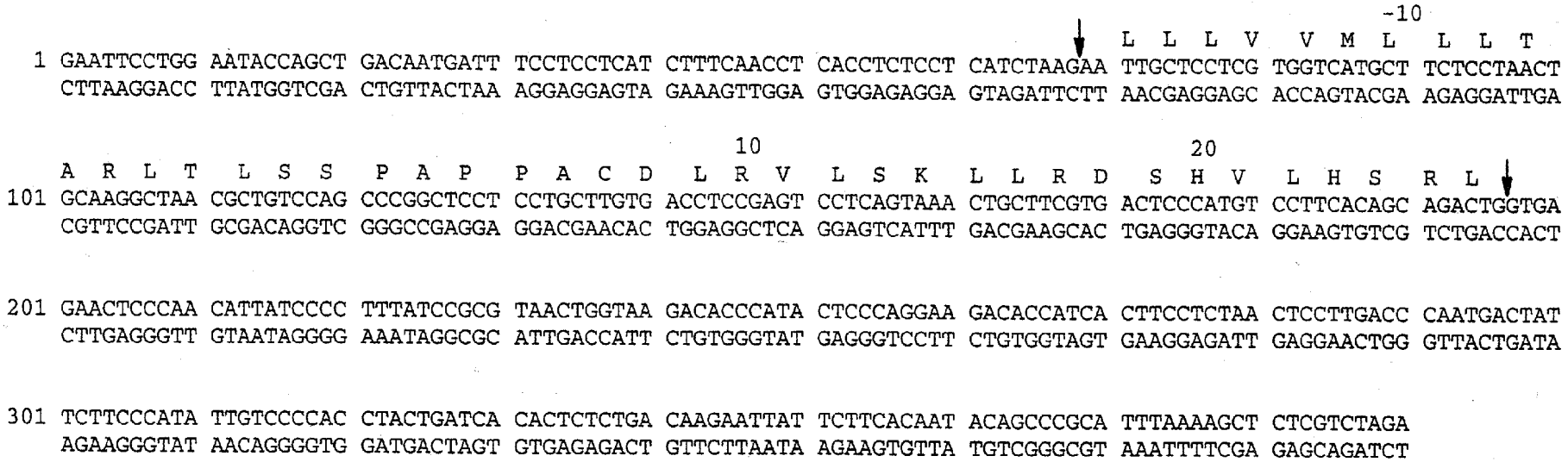

40000
30000
20000
10000
0
125I-HP1-1D Bound
(32856,39625)
(32203,20789)
(5085,4056)
(3858,3817)
No APP
APP
mpl-IgG
ANP-R-IgG

FIG. 7


-10
L L L V V M L L L T
1 GAATTCCTGG AATACCAGCT GACAATGATT TCCTCCTCAT CTTTCAACCT CACCTCTCCT CATCTAAGAA TTGCTCCTCG TGGTCATGCT TCTCCTAACT
CTTAAGGACC TTATGGTCGA CTGTTACTAA AGGAGGAGTA GAAAGTTGGA GTGGAGAGGA GTAGATTCTT AACGAGGAGC ACCAGTACGA AGAGGATTGA
10
20
A R L T L S S P A P P A C D L R V L S K L L R D S H V L H S R L
101 GCAAGGCTAA CGCTGTCCAG CCCGGCTCCT CCTGCTTGTG ACCTCCGAGT CCTCAGTAAA CTGCTTCGTG ACTCCCATGT CCTTCACAGC AGACTGGTGA
CGTTCCGATT GCGACAGGTC GGGCCGAGGA GGACGAACAC TGGAGGCTCA GGAGTCATTT GACGAAGCAC TGAGGGTACA GGAAGTGTCG TCTGACCACT
201 GAACTCCCAA CATTATCCCC TTTATCCGCG TAACTGGTAA GACACCCATA CTCCCAGGAA GACACCATCA CTTCCTCTAA CTCCTTGACC CAATGACTAT
CTTGAGGGTT GTAATAGGGG AAATAGGCGC ATTGACCATT CTGTGGGTAT GAGGGTCCTT CTGTGGTAGT GAAGGAGATT GAGGAACTGG GTTACTGATA
301 TCTTCCCATA TTGTCCCCAC CTACTGATCA CACTCTCTGA CAAGAATTAT TCTTCACAAT ACAGCCCGCA TTTAAAAGCT CTCGTCTAGA
AGAAGGGTAT AACAGGGGTG GATGACTAGT GTGAGAGACT GTTCTTAATA AGAAGTGTTA TGTCGGGCGT AAATTTTCGA GAGCAGATCT


1 GCGTCTTCCT ACCCATCTGC TCCCCAGAGG GCTGCCTGCT GTGCACTTGG GTCCTGGAGC CCTTCTCCAC CCGGATAGAT TCCTCACCCT TGGCCCGCCT
CGCAGAAGGA TGGGTAGACG AGGGGTCTCC CGACGGACGA CACGTGAACC CAGGACCTCG GGAAGAGGTG GGCCTATCTA AGGAGTGGGA ACCGGGCGGA
101 TTGCCCCACC CTACTCTGCC CAGAAGTGCA AGAGCCTAAG CCGCCTCCAT GGCCCCAGGA AGGATTCAGG GGAGAGGCCC CAAACAGGGA GCCACGCCAG
AACGGGGTGG GATGAGACGG GTCTTCACGT TCTCGGATTC GGCGGAGGTA CCGGGGTCCT TCCTAAGTCC CCTCTCCGGG GTTTGTCCCT CGGTGCGGTC
-20 -10 1
Me tGluLeuThr GluLeuLeuL euValValMe tLeuLeuLeu ThrAlaArgL euThrLeuSe rSerProAla ProProAlaCys
201 CCAGACACCC CGGCCAGAAT GGAGCTGACT GAATTGCTCC TCGTGGTCAT GCTTCTCCTA ACTGCAAGGC TAACGCTGTC CAGCCCGGCT CCTCCTGCTT
GGTCTGTGGG GCCGGTCTTA CCTCGACTGA CTTAACGAGG AGCACCAGTA CGAAGAGGAT TGACGTTCCG ATTGCGACAG GTCGGGCCGA GGAGGACGAA
10 20 30 40
AspLeuAr gValLeuSer LysLeuLeuA rgAspSerHi sValLeuHis SerArgLeuS erGlnCysPr oGluValHis ProLeuProT hrProValLeu
301 GTGACCTCCG AGTCCTCAGT AAACTGCTTC GTGACTCCCA TGTCCTTCAC AGCAGACTGA GCCAGTGCCC AGAGGTTCAC CCTTTGCCTA CACCTGTCCT
CACTGGAGGC TCAGGAGTCA TTTGACGAAG CACTGAGGGT ACAGGAAGTG TCGTCTGACT CGGTCACGGG TCTCCAAGTG GGAAACGGAT GTGGACAGGA
50 60 70
LeuProAla ValAspPheS erLeuGlyGl uTrpLysThr GlnMetGluG luThrLysAl aGlnAspIle LeuGlyAlaV alThrLeuLe uLeuGluGly
401 GCTGCCTGCT GTGGACTTTA GCTTGGGAGA ATGGAAAACC CAGATGGAGG AGACCAAGGC ACAGGACATT CTGGGAGCAG TGACCCTTCT GCTGGAGGGA
CGACGGACGA CACCTGAAAT CGAACCCTCT TACCTTTTGG GTCTACCTCC TCTGGTTCCG TGTCCTGTAA GACCCTCGTC ACTGGGAAGA CGACCTCCCT
80 90 100
ValMetAlaA laArgGlyGl nLeuGlyPro ThrCysLeuS erSerLeuLe uGlyGlnLeu SerGlyGlnV alArgLeuLe uLeuGlyAla LeuGlnSerLeu
501 GTGATGGCAG CACGGGGACA ACTGGGACCC ACTTGCCTCT CATCCCTCCT GGGGCAGCTT TCTGGACAGG TCCGTCTCCT CCTTGGGGCC CTGCAGAGCC
CACTACCGTC GTGCCCCTGT TGACCCTGGG TGAACGGAGA GTAGGGAGGA CCCCGTCGAA AGACCTGTCC AGGCAGAGGA GGAACCCCGG GACGTCTCGG
110 120 130 140
LeuGlyTh rGlnLeuPro ProGlnGlyA rgThrThrAl aHisLysAsp ProAsnAlaI lePheLeuSe rPheGlnHis LeuLeuArgG lyLysValArg
601 TCCTTGGAAC CCAGCTTCCT CCACAGGGCA GGACCACAGC TCACAAGGAT CCCAATGCCA TCTTCCTGAG CTTCCAACAC CTGCTCCGAG GAAAGGTGCG
AGGAACCTTG GGTCGAAGGA GGTGTCCCGT CCTGGTGTCG AGTGTTCCTA GGGTTACGGT AGAAGGACTC GAAGGTTGTG GACGAGGCTC CTTTCCACGC
150 160 170
PheLeuMet LeuValGlyG lySerThrLe uCysValArg ArgAlaProP roThrThrAl aValProSer ArgThrSerL euValLeuTh rLeuAsnGlu
701 TTTCCTGATG CTTGTAGGAG GGTCCACCCT CTGCGTCAGG CGGGCCCCAC CCACCACAGC TGTCCCCAGC AGAACCTCTC TAGTCCTCAC ACTGAACGAG
AAAGGACTAC GAACATCCTC CCAGGTGGGA GACGCAGTCC GCCCGGGGTG GGTGGTGTCG ACAGGGGTCG TCTTGGAGAG ATCAGGAGTG TGACTTGCTC
180 190 200
LeuProAsnA rgThrSerGl yLeuLeuGlu ThrAsnPheT hrAlaSerAl aArgThrThr GlySerGlyL euLeuLysTr pGlnGlnGly PheArgAlaLys
801 CTCCCAAACA GGACTTCTGG ATTGTTGGAG ACAAACTTCA CTGCCTCAGC CAGAACTACT GGCTCTGGGC TTCTGAAGTG GCAGCAGGGA TTCAGAGCCA
GAGGGTTTGT CCTGAAGACC TAACAACCTC TGTTTGAAGT GACGGAGTCG GTCTTGATGA CCGAGACCCG AAGACTTCAC CGTCGTCCCT AAGTCTCGGT

Figure 8a

```
          210                                 220                                 230                                 240
       IleProGl yLeuLeuAsn GlnThrSerA rgSerLeuAs pGlnIlePro GlyTyrLeuA snArgIleHi sGluLeuLeu AsnGlyThrA rgGlyLeuPhe
 901 AGATTCCTGG TCTGCTGAAC CAAACCTCCA GGTCCCTGGA CCAAATCCCC GGATACCTGA ACAGGATACA CGAACTCTTG AATGGAACTC GTGGACTCTT
     TCTAAGGACC AGACGACTTG GTTTGGAGGT CCAGGGACCT GGTTTAGGGG CCTATGGACT TGTCCTATGT GCTTGAGAAC TTACCTTGAG CACCTGAGAA

                               250                                 260                                 270
      ProGlyPro SerArgArgT hrLeuGlyAl aProAspIle SerSerGlyT hrSerAspTh rGlySerLeu ProProAsnL euGlnProGl yTyrSerPro
1001 TCCTGGACCC TCACGCAGGA CCCTAGGAGC CCCGGACATT TCCTCAGGAA CATCAGACAC AGGCTCCCTG CCACCCAACC TCCAGCCTGG ATATTCTCCT
     AGGACCTGGG AGTGCGTCCT GGGATCCTCG GGGCCTGTAA AGGAGTCCTT GTAGTCTGTG TCCGAGGGAC GGTGGGTTGG AGGTCGGACC TATAAGAGGA

                     280                                 290                                 300
     SerProThrH isProProTh rGlyGlnTyr ThrLeuPheP roLeuProPr oThrLeuPro ThrProValV alGlnLeuHi sProLeuLeu ProAspProSer
1101 TCCCCAACCC ATCCTCCTAC TGGACAGTAT ACGCTCTTCC CTCTTCCACC CACCTTGCCC ACCCCTGTGG TCCAGCTCCA CCCCCTGCTT CCTGACCCTT
     AGGGGTTGGG TAGGAGGATG ACCTGTCATA TGCGAGAAGG GAGAAGGTGG GTGGAACGGG TGGGGACACC AGGTCGAGGT GGGGGACGAA GGACTGGGAA

          310                                 320                                 330
       AlaProTh rProThrPro ThrSerProL euLeuAsnTh rSerTyrThr HisSerGlnA snLeuSerGl nGluGly
1201 CTGCTCCAAC GCCCACCCCT ACCAGCCCTC TTCTAAACAC ATCCTACACC CACTCCCAGA ATCTGTCTCA GGAAGGGTAA GGTTCTCAGA CACTGCCGAC
     GACGAGGTTG CGGGTGGGGA TGGTCGGGAG AAGATTTGTG TAGGATGTGG GTGAGGGTCT TAGACAGAGT CCTTCCCATT CCAAGAGTCT GTGACGGCTG

1301 ATCAGCATTG TCTCATGTAC AGCTCCCTTC CCTGCAGGGC GCCCCTGGGA GACAACTGGA CAAGATTTCC TACTTTCTCC TGAAACCCAA AGCCCTGGTA
     TAGTCGTAAC AGAGTACATG TCGAGGGAAG GGACGTCCCG CGGGGACCCT CTGTTGACCT GTTCTAAAGG ATGAAAGAGG ACTTTGGGTT TCGGGACCAT

1401 AAAGGGATAC ACAGGACTGA AAAGGGAATC ATTTTTCACT GTACATTATA AACCTTCAGA AGCTATTTTT TTAAGCTATC AGCAATACTC ATCAGAGCAG
     TTTCCCTATG TGTCCTGACT TTTCCCTTAG TAAAAAGTGA CATGTAATAT TTGGAAGTCT TCGATAAAAA AATTCGATAG TCGTTATGAG TAGTCTCGTC

1501 CTAGCTCTTT GGTCTATTTT CTGCAGAAAT TTGCAACTCA CTGATTCTCT ACATGCTCTT TTTCTGTGAT AACTCTGCAA AGGCCTGGGC TGGCCTGGCA
     GATCGAGAAA CCAGATAAAA GACGTCTTTA AACGTTGAGT GACTAAGAGA TGTACGAGAA AAAGACACTA TTGAGACGTT TCCGGACCCG ACCGGACCGT

1601 GTTGAACAGA GGGAGAGACT AACCTTGAGT CAGAAAACAG AGAAAGGGTA ATTTCCTTTG CTTCAAATTC AAGGCCTTCC AACGCCCCCA TCCCCTTTAC
     CAACTTGTCT CCCTCTCTGA TTGGAACTCA GTCTTTTGTC TCTTTCCCAT TAAAGGAAAC GAAGTTTAAG TTCCGGAAGG TTGCGGGGGT AGGGGAAATG

1701 TATCATTCTC AGTGGGACTC TGATCCCATA TTCTTAACAG ATCTTTACTC TTGAGAAATG AATAAGCTTT CTCTCAGAAA AAAAAAAAAA AAAAAAAA
     ATAGTAAGAG TCACCCTGAG ACTAGGGTAT AAGAATTGTC TAGAAATGAG AACTCTTTAC TTATTCGAAA GAGAGTCTTT TTTTTTTTTT TTTTTTTT
```

Figure 8b

```
hmpll    1  .....MELTE[LLL]VVML[L]LTARLT[L]SS[P]APPA[CD]L[RVL]SKL[L]RDSHVLH
hepo     1  MGVHECPAWLW[LLL]SLLS[L]PLGLPV[L]GA[P]PRLI[CD]S[RVL]ERY[L]LEAKEAE

hmpll   45  SRLSQ[C]P[E]VHP[L]PTPVLL[P]AVDFSLGE[WK]TQMEETK[A]QDILGAVT[LL]L[E]G
hepo    51  NITTG[C]A[E]HCS[L]NENITV[P]DTKVNFYA[WK]RMEVGQQ[A]VEVWQGLA[LL]S[E]A

hmpll   95  [V]MAARGQ[L]GPTCLS..S[L]LGQLSGQ[V]RL[L]..[L]GA[L]QSL[LG]T[Q]...LP[P]QG
hepo   101  [V]LRGQAL[L]VNSSQPWEP[L]QLHVDKA[V]SG[L]RS[L]TT[L]LRA[LG]A[Q]KEAIS[P]PD

hmpll  138  RTT[A]HKDPNAIFLS[F]QH[L]L[R]GKVR[FL]...MLVGGSTL[C]VRRAPPTTAVPS
hepo   151  AAS[A]APLRTITADT[F]RK[L]F[R]VYSN[FL]RGKLKLYTGEA[C]RTGDR

hmpll  185  RTSLVLTLNELPNRTSGLLETNFTASARTTGSGLLKWQQGFRAKIPGLLN

hmpll  235  QTSRSLDQIPGYLNRIHELLNGTRGLFPGPSRRTLGAPDISSGTSDTGSL

hmpll  285  PPNLQPGYSPSPTHPPTGQYTLFPLPPTLPTPVVQLHPLLPDPSAPTPTP

hmpll  335  TSPLLNTSYTHSQNLSQEG
```

Figure 9

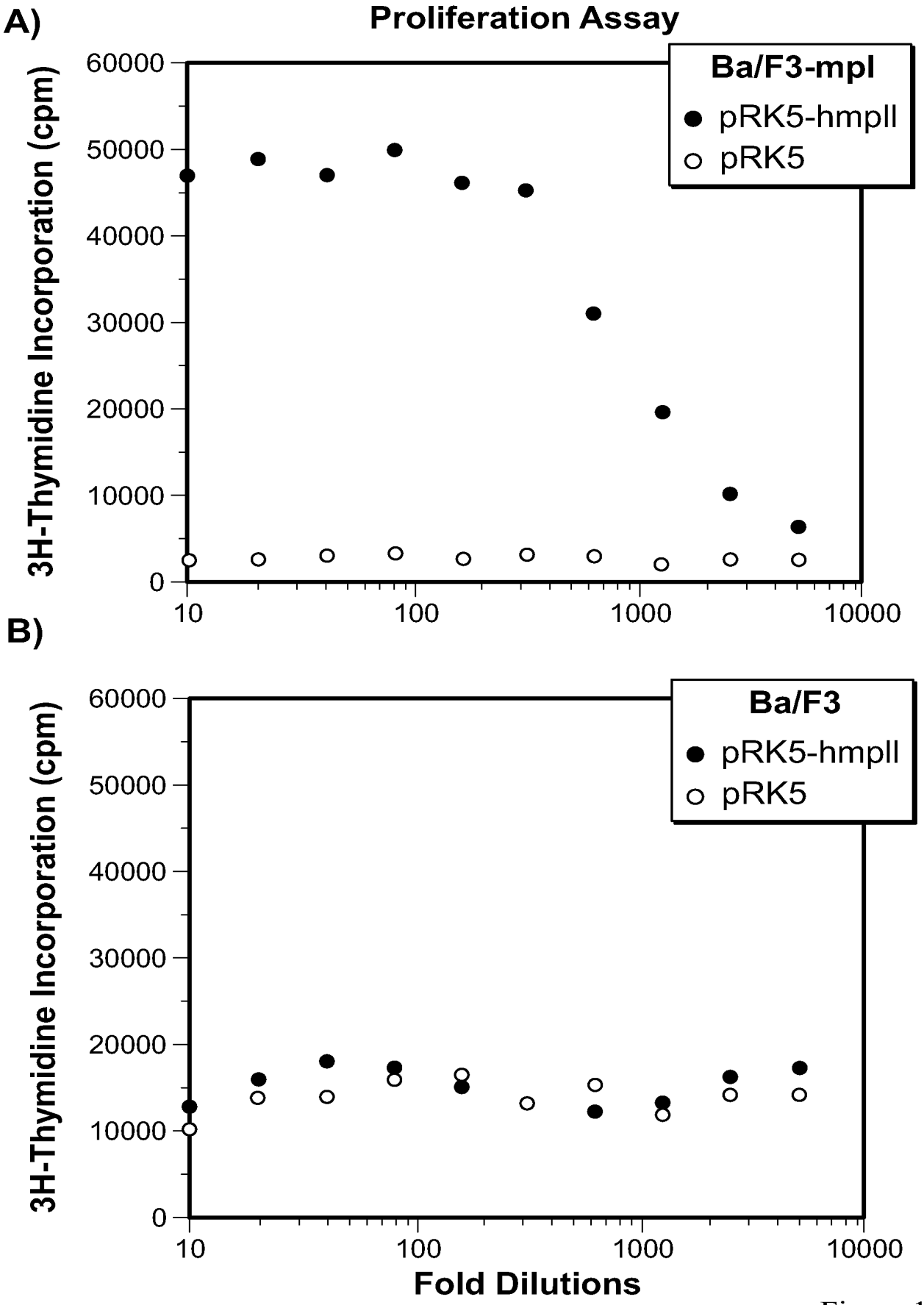

A)
Proliferation Assay
Ba/F3-mpl
pRK5-hmpll
pRK5
3H-Thymidine Incorporation (cpm)
60000
50000
40000
30000
20000
10000
0
10
100
1000
10000
B)
Ba/F3
pRK5-hmpll
pRK5
3H-Thymidine Incorporation (cpm)
60000
50000
40000
30000
20000
10000
0
10
100
1000
10000
Fold Dilutions

Figure 10